Timothy A Thornton

List of Publications by Year
in descending order

82 papers	6,449 citations	136740 32 h-index	91712 69 g-index
91 all docs	91 docs citations	91 times ranked	12098 citing authors

#	Article	IF	Citations
1	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
2	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	13.7	679
3	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. American Journal of Human Genetics, 2016, 98, 653-666.	2.6	347
4	Model-free Estimation of Recent Genetic Relatedness. American Journal of Human Genetics, 2016, 98, 127-148.	2.6	331
5	Robust Inference of Population Structure for Ancestry Prediction and Correction of Stratification in the Presence of Relatedness. Genetic Epidemiology, 2015, 39, 276-293.	0.6	330
6	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2016, 98, 165-184.	2.6	266
7	Genetic association testing using the GENESIS R/Bioconductor package. Bioinformatics, 2019, 35, 5346-5348.	1.8	260
8	Estimating Kinship in Admixed Populations. American Journal of Human Genetics, 2012, 91, 122-138.	2.6	207
9	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	1.5	203
10	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	4.1	191
11	Case-Control Association Testing with Related Individuals: A More Powerful Quasi-Likelihood Score Test. American Journal of Human Genetics, 2007, 81, 321-337.	2.6	183
12	Transethnic genomeâ€wide scan identifies novel Alzheimer's disease loci. Alzheimer's and Dementia, 2017, 13, 727-738.	0.4	166
13	ROADTRIPS: Case-Control Association Testing with Partially or Completely Unknown Population and Pedigree Structure. American Journal of Human Genetics, 2010, 86, 172-184.	2.6	153
14	Dissecting Vancomycin-Intermediate Resistance in Staphylococcus aureus Using Genome-Wide Association. Genome Biology and Evolution, 2014, 6, 1174-1185.	1.1	132
15	Genome-wide Characterization of Shared and Distinct Genetic Components that Influence Blood Lipid Levels in Ethnically Diverse Human Populations. American Journal of Human Genetics, 2013, 92, 904-916.	2.6	113
16	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 886-897.	2.5	107
17	Generalizing polygenic risk scores from Europeans to Hispanics/Latinos. Genetic Epidemiology, 2019, 43, 50-62.	0.6	89
18	Local ancestry at APOE modifies Alzheimer's disease risk in Caribbean Hispanics. Alzheimer's and Dementia, 2019, 15, 1524-1532.	0.4	75

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19	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	2.6	71
20	Embracing Genetic Diversity to Improve Black Health. New England Journal of Medicine, 2021, 384, 1163-1167.	13.9	71
21	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67
22	Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apneaâ€“related Quantitative Trait Locus in Men. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 391-401.	1.4	65
23	African Ancestryâ€“Specific Alleles and Kidney Disease Risk in Hispanics/Latinos. Journal of the American Society of Nephrology: JASN, 2017, 28, 915-922.	3.0	57
24	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. PLoS Genetics, 2017, 13, e1006760.	1.5	53
25	Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke. JAMA Neurology, 2015, 72, 781.	4.5	49
26	Characterizing the Genetic Architecture of Parkinson's Disease in Latinos. Annals of Neurology, 2021, 90, 353-365.	2.8	48
27	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	1.5	45
28	Genome-wide linkage scan and association study of PARL to the expression of LHON families in Thailand. Human Genetics, 2010, 128, 39-49.	1.8	43
29	Whole genome sequencing of Caribbean Hispanic families with lateâ€onset Alzheimer's disease. Annals of Clinical and Translational Neurology, 2018, 5, 406-417.	1.7	42
30	Hepatic Abundance and Activity of Androgen- and Drug-Metabolizing Enzyme UGT2B17 Are Associated with Genotype, Age, and Sex. Drug Metabolism and Disposition, 2018, 46, 888-896.	1.7	42
31	A powerful statistical framework for generalization testing in GWAS, with application to the HCHS/SOL. Genetic Epidemiology, 2017, 41, 251-258.	0.6	41
32	Polymorphic Human Sulfotransferase 2A1 Mediates the Formation of 25-Hydroxyvitamin D₃-3-O-Sulfate, a Major Circulating Vitamin D Metabolite in Humans. Drug Metabolism and Disposition, 2018, 46, 367-379.	1.7	41
33	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	1.4	41
34	On the cross-population generalizability of gene expression prediction models. PLoS Genetics, 2020, 16, e1008927.	1.5	41
35	Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. Human Molecular Genetics, 2017, 26, 1193-1204.	1.4	38
36	Powerful Genetic Association Analysis for Common or Rare Variants with High-Dimensional Structured Traits. Genetics, 2017, 206, 1779-1790.	1.2	36

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37	Accuracy of Gene Expression Prediction From Genotype Data With PrediXcan Varies Across and Within Continental Populations. Frontiers in Genetics, 2019, 10, 261.	1.1	36
38	Admixture Mapping Identifies an Amerindian Ancestry Locus Associated with Albuminuria in Hispanics in the United States. Journal of the American Society of Nephrology: JASN, 2017, 28, 2211-2220.	3.0	33
39	Genome-wide association study of iron traits and relation to diabetes in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL): potential genomic intersection of iron and glucose regulation?. Human Molecular Genetics, 2017, 26, 1966-1978.	1.4	31
40	Genome-wide association study of dental caries in the Hispanic Communities Health Study/Study of Latinos (HCHS/SOL). Human Molecular Genetics, 2016, 25, 807-816.	1.4	29
41	Admixture mapping in the Hispanic Community Health Study/Study of Latinos reveals regions of genetic associations with blood pressure traits. PLoS ONE, 2017, 12, e0188400.	1.1	29
42	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	1.5	28
43	XM: Association Testing on the Xâ€Chromosome in Caseâ€Control Samples With Related Individuals. Genetic Epidemiology, 2012, 36, 438-450.	0.6	27
44	Adiponectin pathway polymorphisms and risk of breast cancer in African Americans and Hispanics in the Womenâ€™s Health Initiative. Breast Cancer Research and Treatment, 2013, 139, 461-468.	1.1	27
45	Identification of a prostate cancer susceptibility gene on chromosome 5p13q12 associated with risk of both familial and sporadic disease. European Journal of Human Genetics, 2009, 17, 368-377.	1.4	26
46	Genetics, Diet, and Season Are Associated with Serum 25-Hydroxycholecalciferol Concentration in a Yupâ€™ik Study Population from Southwestern Alaska. Journal of Nutrition, 2016, 146, 318-325.	1.3	25
47	Genome-wide Significance Thresholds for Admixture Mapping Studies. American Journal of Human Genetics, 2019, 104, 454-465.	2.6	25
48	Improved imputation accuracy in Hispanic/Latino populations with larger and more diverse reference panels: applications in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Human Molecular Genetics, 2016, 25, 3245-3254.	1.4	23
49	Genome-wide association and admixture analysis of glaucoma in the Women's Health Initiative. Human Molecular Genetics, 2014, 23, 6634-6643.	1.4	22
50	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimerâ€™s Disease Sequencing Project. Dementia and Geriatric Cognitive Disorders, 2018, 45, 1-17.	0.7	22
51	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.3	18
52	Coagulation factor VIII: Relationship to cardiovascular disease risk and whole genome sequence and epigenomeâ€wide analysis in African Americans. Journal of Thrombosis and Haemostasis, 2020, 18, 1335-1347.	1.9	17
53	Genetic variations and risk of placental abruption: A genome-wide association study and meta-analysis of genome-wide association studies. Placenta, 2018, 66, 8-16.	0.7	15
54	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157.	2.7	14

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55	Admixture mapping reveals the association between Native American ancestry at 3q13.11 and reduced risk of Alzheimerâ€™s disease in Caribbean Hispanics. Alzheimer's Research and Therapy, 2021, 13, 122.	3.0	14
56	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	2.6	14
57	Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341.	1.1	13
58	Interferon gamma-induced protein 10 (IP-10) and cardiovascular disease in African Americans. PLoS ONE, 2020, 15, e0231013.	1.1	12
59	Genomeâ€Wide Analysis of Copy Number Variation in Latin American Parkinson's Disease Patients. Movement Disorders, 2021, 36, 434-441.	2.2	12
60	The executive prominent/memory prominent spectrum in Alzheimer's disease is highly heritable. Neurobiology of Aging, 2016, 41, 115-121.	1.5	11
61	Application of a New Method for GWAS in a Related Case/Control Sample with Known Pedigree Structure: Identification of New Loci for Nephrolithiasis. PLoS Genetics, 2011, 7, e1001281.	1.5	10
62	Detecting Heterogeneity in Population Structure Across the Genome in Admixed Populations. Genetics, 2016, 204, 43-56.	1.2	10
63	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. Journal of Medical Genetics, 2017, 54, 313-323.	1.5	9
64	Association of DXA-derived Bone Mineral Density and Fat Mass With African Ancestry. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E713-E717.	1.8	8
65	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. PLoS ONE, 2019, 14, e0217796.	1.1	8
66	Sleep problems and risk of cancer incidence and mortality in an older cohort: The Cardiovascular Health Study (CHS). Cancer Epidemiology, 2022, 76, 102057.	0.8	7
67	In Vivo Functional Effects of CYP2C9 M1L, a Novel and Common Variant in the Yupâ€™ik Alaska Native Population. Drug Metabolism and Disposition, 2021, 49, 345-352.	1.7	5
68	Soluble CD14 Levels in the Jackson Heart Study: Associations With Cardiovascular Disease Risk and Genetic Variants. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, e369-e378.	1.1	5
69	Dietary and genetic influences on hemostasis in a Yupâ€™ik Alaska Native population. PLoS ONE, 2017, 12, e0173616.	1.1	5
70	Identity-by-descent estimation with population- and pedigree-based imputation in admixed family data. BMC Proceedings, 2016, 10, 295-301.	1.8	4
71	Estimating relationships between phenotypes and subjects drawn from admixed families. BMC Proceedings, 2016, 10, 357-362.	1.8	4
72	Analysis of pedigree data in populations with multiple ancestries: Strategies for dealing with admixture in Caribbean Hispanic families from the ADSP. Genetic Epidemiology, 2018, 42, 500-515.	0.6	3

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73	Genome-wide association study in the Taiwan Biobank identifies four novel genes for human height: NABP2, RASA2, RNF41 and SLC39A5. Human Molecular Genetics, 2021, 30, 2362-2369.	1.4	3
74	Nicotine metabolism and its association with CYP2A6 genotype among Indigenous people in Alaska who smoke. Clinical and Translational Science, 2021, 14, 2474-2486.	1.5	2
75	Associating sleep problems with advanced cancer diagnosis, and immune checkpoint treatment outcomes: a pilot study. Supportive Care in Cancer, 2022, 30, 3829-3838.	1.0	2
76	REHE: Fast variance components estimation for linear mixed models. Genetic Epidemiology, 2021, 45, 891-905.	0.6	1
77	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
78	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
79	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
80	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
81	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
82	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0